

SEQUENCE LISTING

SEQ ID NO: 1

SEQUENCE LENGTH: 1703

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL SEQUENCE: No

ANTI-SENSE: No

ORIGINAL SOURCE

ORGANISM: *Gentiana triflora* var. *japonica*

TISSUE TYPE: petal

IMMEDIATE SOURCE

LIBRARY: cDNA library

CLONE: pGAT4

SEQUENCE DESCRIPTION

TCATT ATG GAG CAA ATC CAA ATG GTG AAG GTT CTT GAA AAA TGC CAA 47  
Met Glu Gln Ile Gln Met Val Lys Val Leu Glu Lys Cys Gln  
-1 1 5 10  
GTT ACA CCA CCA TCT GAC ACA ACA GAT GTC GAG TTA TCG CTA CCG GTA 95  
Val Thr Pro Pro Ser Asp Thr Thr Asp Val Glu Leu Ser Leu Pro Val  
15 20 25  
ACA TTC TTC GAT ATC CCC TGG TTG CAC TTG AAT AAG ATG CAG TCC CTT 143  
Thr Phe Phe Asp Ile Pro Trp Leu His Leu Asn Lys Met Gln Ser Leu  
30 35 40 45  
CTG TTT TAC GAC TTT CCG TAC CCA AGA ACA CAT TTC TTG GAC ACT GTT 191  
Leu Phe Tyr Asp Phe Pro Tyr Pro Arg Thr His Phe Leu Asp Thr Val  
50 55 60  
ATC CCT AAT CTT AAG GCC TCT TTG TCT CTC ACT CTA AAA CAC TAC GTT 239  
Ile Pro Asn Leu Lys Ala Ser Leu Ser Leu Thr Leu Lys His Tyr Val  
65 70 75  
CCG CTT AGC GGA AAT TTG TTG ATG CCG ATC AAA TCG GGC GAA ATG CCG 287  
Pro Leu Ser Gly Asn Leu Leu Met Pro Ile Lys Ser Gly Glu Met Pro  
80 85 90  
AAG TTT CAG TAC TCC CGT GAT GAG GGC GAC TCG ATA ACT TTG ATC GTT 335  
Lys Phe Gln Tyr Ser Arg Asp Glu Gly Asp Ser Ile Thr Leu Ile Val  
95 100 105

GCG GAG TCT GAC CAG GAT TTT GAC TAC CTT AAA GGT CAT CAA CTG GTA	383
Ala Glu Ser Asp Gln Asp Phe Asp Tyr Leu Lys Gly His Gln Leu Val	
110 115 120 125	
GAT TCC AAT GAT TTG CAT GGC CTT TTT TAT GTT ATG CCA CGG GTT ATA	431
Asp Ser Asn Asp Leu His Gly Leu Phe Tyr Val Met Pro Arg Val Ile	
130 135 140	
AGG ACC ATG CAA GAC TAT AAA GTG ATC CCG CTC GTA GCC GTG CAA GTA	479
Arg Thr Met Gln Asp Tyr Lys Val Ile Pro Leu Val Ala Val Gln Val	
145 150 155	
ACC GTT TTT CCT AAC CGT GGC ATA GCC GTG GCT CTG ACG GCA CAT CAT	527
Thr Val Phe Pro Asn Arg Gly Ile Ala Val Ala Leu Thr Ala His His	
160 165 170	
TCA ATT GCA GAT GCT AAA AGT TTT GTA ATG TTC ATC AAT GCT TGG GCC	575
Ser Ile Ala Asp Ala Lys Ser Phe Val Met Phe Ile Asn Ala Trp Ala	
175 180 185	
TAT ATT AAC AAA TTT GGG AAA GAC GCG GAC TTG TTG TCC GCG AAT CTT	623
Tyr Ile Asn Lys Phe Gly Lys Asp Ala Asp Leu Leu Ser Ala Asn Leu	
190 195 200 205	
CTT CCA TCT TTC GAT AGA TCG ATA ATC AAA GAT CTG TAT GGC CTA GAG	671
Leu Pro Ser Phe Asp Arg Ser Ile Ile Lys Asp Leu Tyr Gly Leu Glu	
210 215 220	
GAA ACA TTT TGG AAC GAA ATG CAA GAT GTT CTT GAA ATG TTC TCT AGA	719
Glu Thr Phe Trp Asn Glu Met Gln Asp Val Leu Glu Met Phe Ser Arg	
225 230 235	
TTT GGA AGC AAA CCC CCT CGA TTC AAC AAG GTA CGA GCT ACA TAT GTC	767
Phe Gly Ser Lys Pro Pro Arg Phe Asn Lys Val Arg Ala Thr Tyr Val	
240 245 250	
CTC TCC CTT GCT GAA ATC CAG AAG CTA AAG AAC AAA GTA CTG AAT CTC	815
Leu Ser Leu Ala Glu Ile Gln Lys Leu Lys Asn Lys Val Leu Asn Leu	
255 260 265	
AGA GGA TCC GAA CCG ACA ATA CGT GTA ACG ACG TTC ACA ATG ACG TGT	863
Arg Gly Ser Glu Pro Thr Ile Arg Val Thr Thr Phe Thr Met Thr Cys	
270 275 280 285	
GGA TAC GTA TGG ACA TGC ATG GTC AAA TCA AAA GAT GAC GTC GTA TCA	911
Gly Tyr Val Trp Thr Cys Met Val Lys Ser Lys Asp Asp Val Val Ser	
290 295 300	

GAG GAA TCA TCG AAC GAC GAA AAT GAG CTC GAG TAC TTC AGT TTT ACA	959
Glu Glu Ser Ser Asn Asp Glu Asn Glu Leu Glu Tyr Phe Ser Phe Thr	
305 310 315	
GCG GAT TGC CGA GGA CTT CTG ACG CCC CCG TGT CCG CCT AAC TAC TTT	1007
Ala Asp Cys Arg Gly Leu Leu Thr Pro Pro Cys Pro Pro Asn Tyr Phe	
320 325 330	
GGC AAC TGT CTT GCG TCA TGC GTT GCA AAA GCA ACA CAT AAA GAG TTA	1055
Gly Asn Cys Leu Ala Ser Cys Val Ala Lys Ala Thr His Lys Glu Leu	
335 340 345	
GTT GGG GAT AAA GGG CTT CTT GTT GCA GTT GCA GCT ATT GGA GAA GCC	1103
Val Gly Asp Lys Gly Leu Leu Val Ala Val Ala Ala Ile Gly Glu Ala	
350 355 360 365	
ATT GAA AAG AGG TTG CAC AAC GAA AAA GGC GTT CTT GCA GAT GCA AAA	1151
Ile Glu Lys Arg Leu His Asn Glu Lys Gly Val Leu Ala Asp Ala Lys	
370 375 380	
ACT TGG TTA TCG GAA TCT AAT GGA ATC CCT TCA AAA AGA TTT CTC GGG	1199
Thr Trp Leu Ser Glu Ser Asn Gly Ile Pro Ser Lys Arg Phe Leu Gly	
385 390 395	
ATT ACC GGA TCG CCT AAG TTC GAT TCG TAT GGT GTA GAT TTT GGA TGG	1247
Ile Thr Gly Ser Pro Lys Phe Asp Ser Tyr Gly Val Asp Phe Gly Trp	
400 405 410	
GGA AAG CCT GCA AAA TTT GAC ATT ACC TCT GTT GAT TAT GCA GAA TTG	1295
Gly Lys Pro Ala Lys Phe Asp Ile Thr Ser Val Asp Tyr Ala Glu Leu	
415 420 425	
ATT TAT GTG ATT CAG TCC AGG GAT TTT GAA AAA GGT GTG GAG ATT GGA	1343
Ile Tyr Val Ile Gln Ser Arg Asp Phe Glu Lys Gly Val Glu Ile Gly	
430 435 440 445	
GTA TCA TTG CCT AAG ATT CAT ATG GAT GCA TTT GCA AAA ATC TTT GAA	1391
Val Ser Leu Pro Lys Ile His Met Asp Ala Phe Ala Lys Ile Phe Glu	
450 455 460	
GAA GGC TTT TGC TCT TTG TCA TAGTCTCTTT AATAGAACCA TATTTGCTGC	1442
Glu Gly Phe Cys Ser Leu Ser	
465 468	
AATAAAGTAC CAAGTCCTTT AGTAACACTA CACCAAACCC TACTTTTCGAG GCGGGAACAC	1502
CACAACGAGG TTCAATCACT AGAAGGTTGT ACTTCATAAA TTCCAGAGGT CGAATATACA	1562
CCGTTGTCCT CTGAAAAGTT GAACCTCACA CCTGACATGG TGTTACGATA GGTATTGTAT	1622
AATGCCATTA TATACTTCCA TAAAGTATCC TATGCAATAG AGAACATGTT ATGTGTTAAA	1682

AAAAAAAAAA AAAAAAAAAA A

1703

SEQ ID NO: 2

SEQUENCE LENGTH: 1622

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL SEQUENCE: No

ANTI-SENSE: No

ORIGINAL SOURCE

ORGANISM: *Gentiana triflora* var. *japonica*

TISSUE TYPE: petal

IMMEDIATE SOURCE

LIBRARY: cDNA library

CLONE: pGAT106

SEQUENCE DESCRIPTION

GAACCATTGA ATCCAATTAA TCTGATTAT TAAG ATG GCA GGA AAT TCC GAG 52

Met Ala Gly Asn Ser Glu

1

5

GAT ATC AAA GTT CTT GAG AAA TGC CGT GTT GCG CCA CCA CCG GAC GCC 100

Asp Ile Lys Val Leu Glu Lys Cys Arg Val Ala Pro Pro Pro Asp Ala

10

15

20

GTC GCC GAG TTT ACA GTC CCA CTG TCG TTT TTC GAC ATG CGA TGG TTG 148

Val Ala Glu Phe Thr Val Pro Leu Ser Phe Phe Asp Met Arg Trp Leu

25

30

35

ATC TCT GAT GCA GAA CAC CAT CTG CAT TTC TAC AGA TTC CGC CAT CCT 196

Ile Ser Asp Ala Glu His His Leu His Phe Tyr Arg Phe Arg His Pro

40

45

50

TGT CCC AAC TCT AAA TTT ATC ATT TCA TCC ATT AAA TCG TCC CTT TCC 244

Cys Pro Asn Ser Lys Phe Ile Ile Ser Ser Ile Lys Ser Ser Leu Ser

55

60

65

70

CTT GTT CTC AAA CAC TTT CTT CCG TTA GCC GGG AAT TTG ATT TGG CCG 292

Leu Val Leu Lys His Phe Leu Pro Leu Ala Gly Asn Leu Ile Trp Pro

75

80

85

GTA GAT TCC TCC GAT AGA ATG CCG GAG TTG CGT TAC AAG AAA GGG GAC 340

Val Asp Ser Ser Asp Arg Met Pro Glu Leu Arg Tyr Lys Lys Gly Asp

90

95

100

TCC GTT TCT TTA ACA ATT GCA GAA TCG AGC ATG GAT TTT GAT TAT CTC	388
Ser Val Ser Leu Thr Ile Ala Glu Ser Ser Met Asp Phe Asp Tyr Leu	
105 110 115	
GCC GGA GAT CAT CAG AGG GAT TCT TAT AAA TTC AAC GAT TTG ATT CCG	436
Ala Gly Asp His Gln Arg Asp Ser Tyr Lys Phe Asn Asp Leu Ile Pro	
120 125 130	
CAG CTG CCA GAA CCG ATT GTA ACC TCC GGC GAC GAA GTA TTA CCA CTT	484
Gln Leu Pro Glu Pro Ile Val Thr Ser Gly Asp Glu Val Leu Pro Leu	
135 140 145 150	
TTT GCT TTA CAG GTG ACG GTG TTC TCC AAC ACC GGT ATA TGC ATT GGA	532
Phe Ala Leu Gln Val Thr Val Phe Ser Asn Thr Gly Ile Cys Ile Gly	
155 160 165	
CGC AAT CTT CAT CAA GTT CTT GGT GAT GCC AGT TCT TTT CTG CAT TTT	580
Arg Asn Leu His Gln Val Leu Gly Asp Ala Ser Ser Phe Leu His Phe	
170 175 180	
AAT AAA TTA TGG GTT TTG GTT GAC AAA TCC AAT GGA GAT TCA TTA AAG	628
Asn Lys Leu Trp Val Leu Val Asp Lys Ser Asn Gly Asp Ser Leu Lys	
185 190 195	
TTC CTT CCA CTT TCT TCT CTA CCT ATG TAC GAC AGA TCT GTG GTG CAA	676
Phe Leu Pro Leu Ser Ser Leu Pro Met Tyr Asp Arg Ser Val Val Gln	
200 205 210	
GAT CCA TTT CAT ATT CCG CGA AAA ATC TAC AAT GAA AGA AAA CTG CTC	724
Asp Pro Phe His Ile Arg Arg Lys Leu Tyr Asn Glu Arg Lys Leu Leu	
215 220 225 230	
AAA TCT CAG GGC ACA CCT ACT GTT CTA AAT CCA GCA ATT TCT AAA GAT	772
Lys Ser Gln Gly Thr Pro Thr Val Leu Asn Pro Ala Ile Ser Lys Asp	
235 240 245	
GAA GTT CGA GCC ACC TTC ATC CTA CAC CCT ATT GAT ATC ATG AAG CTC	820
Glu Val Arg Ala Thr Phe Ile Leu His Pro Ile Asp Ile Met Lys Leu	
250 255 260	
AAG AAA TTC ATT TCG TCA AAA AAT CGC AAC TTA ACC GGT AGT AGT AAT	868
Lys Lys Phe Ile Ser Ser Lys Asn Arg Asn Leu Thr Gly Ser Ser Asn	
265 270 275	
TAT AAT CTG TCA ACT TTC ACG GTG ACA TCT GCA CTG ATC TGG ACA TGC	916
Tyr Asn Leu Ser Thr Phe Thr Val Thr Ser Ala Leu Ile Trp Thr Cys	
280 285 290	

TTG TCG AAA TCA TTA GAC ACC GTC GTA AGA GAG AAG GTG GAA GAG GAT	964
Leu Ser Lys Ser Leu Asp Thr Val Val Arg Glu Lys Val Glu Glu Asp	
295 300 305 310	
AAA CAT GCA GCA AAC TTA TGT GCT TTC ATC AAC TGC CGA CAA CGT TTT	1012
Lys His Ala Ala Asn Leu Cys Ala Phe Ile Asn Cys Arg Gln Arg Phe	
315 320 325	
GCT CCG CCG ATA CCT CAA AAT TAC TTT GGA AAT TGC ATA GTG CCT TGT	1060
Ala Pro Pro Ile Pro Gln Asn Tyr Phe Gly Asn Cys Ile Val Pro Cys	
330 335 340	
ATG GTG GGA TCG ACT CAT GAG CAA CTT GTA GGA AAT GAA GGG TTG TCG	1108
Met Val Gly Ser Thr His Glu Gln Leu Val Gly Asn Glu Gly Leu Ser	
345 350 355	
GTA GCT GCA ACC GCC ATC GGA GAT GCT ATC CAT AAG AGG TTA CAT GAC	1156
Val Ala Ala Thr Ala Ile Gly Asp Ala Ile His Lys Arg Leu His Asp	
360 365 370	
TAC GAA GGA ATT CTG AGA GGA GAT TGG ATA TCG CCG CCC CGA TCA ACA	1204
Tyr Glu Gly Ile Leu Arg Gly Asp Trp Ile Ser Pro Pro Arg Ser Thr	
375 380 385 390	
TCT GCG GCA CCA AGG TCG ACG CTC ATT TAT GTC GTT GGA TCC GCA CAA	1252
Ser Ala Ala Pro Arg Ser Thr Leu Ile Tyr Val Val Gly Ser Ala Gln	
395 400 405	
CGC AAT GTG CAT GAT TTT GAT GCA GAT TTT GGT TGG GGA AAG CTT GAA	1300
Arg Asn Val His Asp Phe Asp Ala Asp Phe Gly Trp Gly Lys Leu Glu	
410 415 420	
AAG CAT GAA TCT GTT TCA ACT AAT CCT TCG GCA ACA CTA ATT TTG ATC	1348
Lys His Glu Ser Val Ser Thr Asp Pro Ser Ala Thr Leu Ile Leu Ile	
425 430 435	
TCT CGG TCC AGA AGA TTT AAA GGA GCA CTT GAG CTT GGC ATT TCT TTG	1396
Ser Arg Ser Arg Arg Phe Lys Gly Ala Leu Glu Leu Gly Ile Ser Leu	
440 445 450	
CCT AAG AAT AGG ATG GAC GCA TTT GCC ACC ATT TTT ACG AAT TTC ATC	1444
Pro Lys Asn Arg Met Asp Ala Phe Ala Thr Ile Phe Thr Asn Phe Ile	
455 460 465 470	
AAT AGT CTC CAT GTG AGG AGC CCT TTG TAAGAAAAAA GTGGTATCAA	1491
Asn Ser Leu His Val Arg Ser Pro Leu	
475 479	
TGTATAAAAA AGACAGACAA GTTATGATGC AACAAATGTT TTAGGAGATT ACAAATCCAT	1551

GGGAAGATGT ATCAAACTCA TCTCTCTATA TATATATATT CAATTGTTTT AAAAAAAAAA 1611  
AAAAAAAAAA A 1622

SEQ ID NO: 3

SEQUENCE LENGTH: 1605

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL SEQUENCE: No

ANTI-SENSE: No

ORIGINAL SOURCE

ORGANISM: Petunia hybrida

TISSUE TYPE: petal

IMMEDIATE SOURCE

LIBRARY: cDNA library

CLONE: pPAT48

SEQUENCE DESCRIPTION

TGTCGACGAA ATCCATTTCA TTTCTCTTC TTTCTTGTTT TTCTAATTC GTCATCATTG 60  
TTATCC ATG GCA GGT GAA GTA GCA AAA CAA GAA GTT ACA AAA GTG AAA 108  
Met Ala Gly Glu Val Ala Lys Gln Glu Val Thr Lys Val Lys  
1 5 10  
GTC CTG AAA AAA ACA AAC GTG AAA CCA CAT AAA CCA CTA GGA AAA AAA 156  
Val Leu Lys Lys Thr Asn Val Lys Pro His Lys Pro Leu Gly Lys Lys  
15 20 25 30  
GAG TGT CAA TTG GTA ACA TTT GAT CTT CCT TAC CTA GCT TTC TAT TAC 204  
Glu Cys Gln Leu Val Thr Phe Asp Leu Pro Tyr Leu Ala Phe Tyr Tyr  
35 40 45  
AAC CAA AAA TTT CTC ATC TAT AAA GGT GCT GAA AAC TTT GAC GAG ACG 252  
Asn Gln Lys Phe Leu Ile Tyr Lys Gly Ala Glu Asn Phe Asp Glu Thr  
50 55 60  
GTG GAA AAA ATT AAA GAT GGA CTG GCC TTA GTA TTG GTG GAT TTC TAT 300  
Val Glu Lys Ile Lys Asp Gly Leu Ala Leu Val Leu Val Asp Phe Tyr  
65 70 75  
CAA CTA GCT GGG AAA CTT GGA AAA GAT GAA GAA GGG GTT TTC AGG GTG 348  
Gln Leu Ala Gly Lys Leu Gly Lys Asp Glu Glu Gly Val Phe Arg Val  
80 85 90

GAA TAC GAC GAT GAC ATG GAT GGT GTA GAG GTG ACA GTG GCT GTT GCA	396
Glu Tyr Asp Asp Asp Met Asp Gly Val Glu Val Thr Val Ala Val Ala	
95 100 105 110	
GAA GAG ATA GAA GTT GCA GAT CTT ACT GAT GAA GAA GGC ACC ACC AAA	444
Glu Glu Ile Glu Val Ala Asp Leu Thr Asp Glu Glu Gly Thr Thr Lys	
115 120 125	
TTC CAG GAC TTG ATT CCT TGT AAT AAA ATC TTG AAT TTG GAA GGG CTT	492
Phe Gln Asp Leu Ile Pro Cys Asn Lys Ile Leu Asn Leu Glu Gly Leu	
130 135 140	
CAT CGC CCT CTT CTA GCT GTG CAG CTC ACC AAG CTC AAG GAC GGG CTC	540
His Arg Pro Leu Leu Ala Val Gln Leu Thr Lys Leu Lys Asp Gly Leu	
145 150 155	
ACC ATG GGA TTA GCA TTT AAC CAT GCT GTG CTG GAT GGT ACT TCG ACG	588
Thr Met Gly Leu Ala Phe Asn His Ala Val Leu Asp Gly Thr Ser Thr	
160 165 170	
TGG CAC TTT ATG ACC TCG TGG TCC GAG CTT TGC TGT GGG TCC ACC TCA	636
Trp His Phe Met Thr Ser Trp Ser Glu Leu Cys Cys Gly Ser Thr Ser	
175 180 185 190	
ATT TCT GTC CCA CCA TTC CTT GAA CGA ACC AAG GCT CGT AAC ACT CGA	684
Ile Ser Val Pro Pro Phe Leu Glu Arg Thr Lys Ala Arg Asn Thr Arg	
195 200 205	
GTC AAG CTC AAC CTC TCT CAA CCA TCA GAT GCA CCC GAA CAT GCT AAG	732
Val Lys Leu Asn Leu Ser Gln Pro Ser Asp Ala Pro Glu His Ala Lys	
210 215 220	
TCA GCA ACC AAC GGT GAT GTC CCG GCC AAC GTA GAC CCA CCT CTT CGC	780
Ser Ala Thr Asn Gly Asp Val Pro Ala Asn Val Asp Pro Pro Leu Arg	
225 230 235	
GAA AGA GTA TTC AAG TTC TCC GAG TTA GCA ATT GAC AAA ATC AAG TCA	828
Glu Arg Val Phe Lys Phe Ser Glu Leu Ala Ile Asp Lys Ile Lys Ser	
240 245 250	
ACA GTC AAT GCC AAC TCA GGA GAG ACG CCA TTC TCC ACA TTC CAA TCA	876
Thr Val Asn Ala Asn Ser Gly Glu Thr Pro Phe Ser Thr Phe Gln Ser	
255 260 265 270	
CTC TCC GCA CAC GTG TGG CTA GCC GTC ACA CGT GCG CGC CAA CTC AAG	924
Leu Ser Ala His Val Trp Leu Ala Val Thr Arg Ala Arg Gln Leu Lys	
275 280 285	



CCC GAG GAC TAC ACT GTG TAC ACT GTG TTT GCT GAT TGC AGG AAA AGG	972
Pro Glu Asp Tyr Thr Val Tyr Thr Val Phe Ala Asp Cys Arg Lys Arg	
290 295 300	
GTT GAT CCT CCA ATG CCA GAA AGT TAC TTC GGC AAC CTA ATT CAG GCA	1020
Val Asp Pro Pro Met Pro Glu Ser Tyr Phe Gly Asn Leu Ile Gln Ala	
305 310 315	
ATT TTC ACA GTG ACC GCG GCA GGT TTG TTA CTA GCA AGC CCG ATC GAG	1068
Ile Phe Thr Val Thr Ala Ala Gly Leu Leu Leu Ala Ser Pro Ile Glu	
320 325 330	
TTC GCT GGT GGG ATG ATA CAA CAA GCG ATC GTG AAG CAT GAC GCT AAG	1116
Phe Ala Gly Gly Met Ile Gln Gln Ala Ile Val Lys His Asp Ala Lys	
335 340 345 350	
GCC ATT GAT CAA AGA AAC AAG GAG TGG GAG AGC AAC CCG AAG ATC TTT	1164
Ala Ile Asp Glu Arg Asn Lys Glu Trp Glu Ser Asn Pro Lys Ile Phe	
355 360 365	
CAG TAC AAA GAT GCT GGA GTG AAC TGT GTT GCT GTT GGA AGT TCG CCA	1212
Gln Tyr Lys Asp Ala Gly Val Asn Cys Val Ala Val Gly Ser Ser Pro	
370 375 380	
AGG TTC AAG GTT TAC GAC GTG GAT TTT GGA TGG GGA AAG CCA GAG AGT	1260
Arg Phe Lys Val Tyr Asp Val Asp Phe Gly Trp Gly Lys Pro Glu Ser	
385 390 395	
GTG AGG AGT GGT TCG AAC AAT AGG TTT GAT GGA ATG GTG TAT TTG TAC	1308
Val Arg Ser Gly Ser Asn Asn Arg Phe Asp Gly Met Val Tyr Leu Tyr	
400 405 410	
CAA GGC AAA AAT GGA GGA AGA AGC ATT GAT GTG GAG ATT AGT TTG GAA	1356
Gln Gly Lys Asn Gly Gly Arg Ser Ile Asp Val Glu Ile Ser Leu Glu	
415 420 425 430	
GCA AAT GCT ATG GAG AGG TTG GAG AAA GAT AAA GAG TTC CTC ATG GAA	1404
Ala Asn Ala Met Glu Arg Leu Glu Lys Asp Lys Glu Phe Leu Met Glu	
435 440 445	
ACT GCT TAATTTGCTT AGCTTGGA CT CAACTGGCTA CACTTTATTT ATGAGCTGCT	1460
Thr Ala	
ATGACTGACA TGCATGTATG TTTATTTTTT TTGGAGGGGT TCTTTCCTTT TATTGTTTTT	1520
TATGTTTTTT CTTTCTTGTA CGTTATGAAG AGAAACCGAG TATAAAGGAA TAATGTTTTT	1580
AGTTATTAAA AAAAAAAAAA AAAAA	1605

SEQ ID NO: 4

SEQUENCE LENGTH: 1479

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL SEQUENCE: No

ANTI-SENSE: No

ORIGINAL SOURCE

ORGANISM: Perilla ocimoides

TISSUE TYPE: leaf

IMMEDIATE SOURCE

LIBRARY: cDNA library

CLONE: pSAT208

SEQUENCE DESCRIPTION

CC GTG ATC GAA ACG TGT AGA GTT GGG CCG CCG CCG GAC TCG GTG GCG	47
Val Ile Glu Thr Cys Arg Val Gly Pro Pro Pro Asp Ser Val Ala	
1 5 10 15	
GAG CAA TCG GTG CCG CTC ACA TTC TTC GAC ATG ACG TGG CTG CAT TTT	95
Glu Gln Ser Val Pro Leu Thr Phe Phe Asp Met Thr Trp Leu His Phe	
20 25 30	
CAT CCC ATG CTT CAG CTC CTC TTC TAC GAA TTC CCT TGT TCC AAG CAA	143
His Pro Met Leu Gln Leu Leu Phe Tyr Glu Phe Pro Cys Ser Lys Gln	
35 40 45	
CAT TTT TCA GAA TCC ATC GTT CCA AAA CTC AAA CAA TCT CTC TCT AAA	191
His Phe Ser Glu Ser Ile Val Pro Lys Leu Lys Gln Ser Leu Ser Lys	
50 55 60	
ACT CTC ATA CAC TTC TTC CCT CTC TCA TGC AAT TTA ATC TAC CCT TCA	239
Thr Leu Ile His Phe Phe Pro Leu Ser Cys Asn Leu Ile Tyr Pro Ser	
65 70 75	
TCC CCG GAG AAA ATG CCG GAG TTT CGG TAT CTA TCC GGG GAC TCG GTT	287
Ser Pro Glu Lys Met Pro Glu Phe Arg Tyr Leu Ser Gly Asp Ser Val	
80 85 90 95	
TCT TTC ACC ATC GCA GAA TCT AGC GAC GAC TTC GAT GAT CTC GTC GGA	335
Ser Phe Thr Ile Ala Glu Ser Ser Asp Asp Phe Asp Asp Leu Val Gly	
100 105 110	
AAT CGT CCA GAA TCT CCC GTT AGG CTC TAC AAC TTT GTC CCT AAA TTG	383
Asn Arg Pro Glu Ser Pro Val Arg Leu Tyr Asn Phe Val Pro Lys Leu	
115 120 125	

CCG CCC ATT GTC GAA GAA TCC GAT AGA AAA CTC TTC CAA GTT TTC GCC	431
Pro Pro Ile Val Glu Glu Ser Asp Arg Lys Leu Phe Gln Val Phe Ala	
130 135 140	
GTG CAG GTG ACT CTT TTC CCA GGC CGA GGC GTC GGT ATT GGA ATA GCA	479
Val Gln Val Thr Leu Phe Pro Gly Arg Gly Val Gly Ile Gly Ile Ala	
145 150 155	
ACG CAT CAC ACC GTT AGC GAC GCC CCG TCG TTT CTC GCG TTT ATA ACG	527
Thr His His Thr Val Ser Asp Ala Pro Ser Phe Leu Ala Phe Ile Thr	
160 165 170 175	
GCT TGG TCT TCA ATG AGC AAA CAC ATT GAA AAT GAA GAT GAA GAT GAA	575
Ala Trp Ser Ser Met Ser Lys His Ile Glu Asn Glu Asp Glu Asp Glu	
180 185 190	
GAA TTT AAA TCT TTG CCA GTT TTC GAT AGA TCC GTC ATA AAA TAT CCG	623
Glu Phe Lys Ser Leu Pro Val Phe Asp Arg Ser Val Ile Lys Tyr Pro	
195 200 205	
ACG AAA TTT GAC TCC ATT TAT TGG AGA AAC GCG CTA AAA TTT CCT TTG	671
Thr Lys Phe Asp Ser Ile Tyr Trp Arg Asn Ala Leu Lys Phe Pro Leu	
210 215 220	
CAA TCT CGT CAT CCC TCA TTA CCG ACG GAC CGC ATT CGA ACC ACG TTC	719
Gln Ser Arg His Pro Ser Leu Pro Thr Asp Arg Ile Arg Thr Thr Phe	
225 230 235	
GTT TTC ACC CAA TCC AAA ATT AAG AAA TTG AAG GGT TGG ATT CAG TCC	767
Val Phe Thr Gln Ser Lys Ile Lys Lys Leu Lys Gly Trp Ile Gln Ser	
240 245 250 255	
AGA GTT CCA AGT TTA GTC CAT CTC TCA TCT TTT GTA GCG ATT GCA GCT	815
Arg Val Pro Ser Leu Val His Leu Ser Ser Phe Val Ala Ile Ala Ala	
260 265 270	
TAT ATG TGG GCT GGC ATA ACG AAA TCA TTC ACA GCA GAT GAA GAC CAA	863
Tyr Met Trp Ala Gly Ile Thr Lys Ser Phe Thr Ala Asp Glu Asp Gln	
275 280 285	
GAC AAC GAG GAT GCA TTT TTC TTG ATT CCG GTC GAT CTA AGG CCA CGA	911
Asp Asn Glu Asp Ala Phe Phe Leu Ile Pro Val Asp Leu Arg Pro Arg	
290 295 300	
TTA GAT CCG CCG GTT CCT GAA AAT TAC TTC GGG AAC TGC TTA TCG TAC	959
Leu Asp Pro Pro Val Pro Glu Asn Tyr Phe Gly Asn Cys Leu Ser Tyr	
305 310 315	

GCG CTG CCG AGA ATG CGG CGG CGA GAG CTG GTG GGA GAG AAA GGG GTG	1007
Ala Leu Pro Arg Met Arg Arg Arg Glu Leu Val Gly Glu Lys Gly Val	
320 325 330 335	
TTT CTG GCA GCT GAG GTA ATC GCG GCG GAG ATA AAA AAA AGC ATC AAC	1055
Phe Leu Ala Ala Glu Val Ile Ala Ala Glu Ile Lys Lys Arg Ile Asn	
340 345 350	
GAC AAG AGA ATA TTA GAA ACG GTG GAG AAA TGG TCG CCG GAG ATT CGT	1103
Asp Lys Arg Ile Leu Glu Thr Val Glu Lys Trp Ser Pro Glu Ile Arg	
355 360 365	
AAA GCG TTG CAG AAA TCA TAT TTT TCG GTG GCA GGA TCG AGC AAG CTA	1151
Lys Ala Leu Gln Lys Ser Tyr Phe Ser Val Ala Gly Ser Ser Lys Leu	
370 375 380	
GAT CTT TAC GGT GCA GAT TTT GGA TGG GGG AAG GCG AGA AAG CAA GAA	1199
Asp Leu Tyr Gly Ala Asp Phe Gly Trp Gly Lys Ala Arg Lys Gln Glu	
385 390 395	
ATA TTG TCG ATT GAT GGG GAG AAA TAT GCA ATG ACR CTT TGT AAA GCC	1247
Ile Leu Ser Ile Asp Gly Glu Lys Tyr Ala Met Thr Leu Cys Lys Ala	
400 405 410 415	
AGG GAT TTC GAA GGA GGA TTG GAG GTT TGC TTG TCT TTG CCT AAG GAC	1295
Arg Asp Phe Glu Gly Gly Leu Glu Val Cys Leu Ser Leu Pro Lys Asp	
420 425 430	
AAA ATG GAT GCT TTT GCT GCT TAT TTT TCA CTG GGA ATT AAT GGT	1340
Lys Met Asp Ala Phe Ala Ala Tyr Phe Ser Leu Gly Ile Asn Gly	
435 440 446	
TAATAAATGT ATGTAATTAA ACTAATATTA TTATGTAACA ATTAATTAAG TGTTGAGTAA	1400
CGTGAAGAAT AATCCCTATT ATATATTTAT GATTTGGTTC AAATAAAGTG TAAAGCCTCT	1460
TGAAAAAAAAAAAAAAAA	1479

SEQ ID NO: 5

SEQUENCE LENGTH: 1508

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL SEQUENCE: No

ANTI-SENSE: No

ORIGINAL SOURCE

ORGANISM: Senecio cruentus

TISSUE TYPE: petal  
IMMEDIATE SOURCE  
LIBRARY: cDNA library  
CLONE: pCAT8

SEQUENCE DESCRIPTION

TG AAC ATT CTC GAA CAT GCC CGA ATA TCG GCC CCC TCG GGC ACC ATC	47
Asn Ile Leu Glu His Ala Arg Ile Ser Ala Pro Ser Gly Thr Ile	
1 5 10 15	
GGC CAT CGC TCG TTA TCT CTT ACT TTC TTC GAC ATT ACT TGG CTA CTC	95
Gly His Arg Ser Leu Ser Leu Thr Phe Phe Asp Ile Thr Trp Leu Leu	
20 25 30	
TTC CCT CCG GTC CAC CAT CTT TTC TTC TAT GAC TTT CCA CAT TCT AAA	143
Phe Pro Pro Val His His Leu Phe Phe Tyr Asp Phe Pro His Ser Lys	
35 40 45	
TCC CAT TTC ATG GAC ACT ATT GTT CCC AGG CTA AAA CAA TCT TTA TCG	191
Ser His Phe Met Asp Thr Ile Val Pro Arg Leu Lys Gln Ser Leu Ser	
50 55 60	
GTC ACT CTT CAA CAT TTT TTC CCG TTT GCT AGT AAT TTG ATT GTA TTT	239
Val Thr Leu Gln His Phe Phe Pro Phe Ala Ser Asn Leu Ile Val Phe	
65 70 75	
CCT AAC ACT GAT GGT TCG GGT TTT AAT AAA AAA CCA GAA ATA AAA CAC	287
Pro Asn Thr Asp Gly Ser Gly Phe Asn Lys Lys Pro Glu Ile Lys His	
80 85 90 95	
GTT GAA GGT GAT TCT GTT GTG GTT ACT TTT GCA GAA TGT TGT CTT GAC	335
Val Glu Gly Asp Ser Val Val Val Thr Phe Ala Glu Cys Cys Leu Asp	
100 105 110	
TTT AAT AAT TTG ACA GGA AAT CAT CCT CGA AAA TGT GAA AAC TTT TAT	383
Phe Asn Asn Leu Thr Gly Asn His Pro Arg Lys Cys Glu Asn Phe Tyr	
115 120 125	
CCA CTT GTA CCT TCA TTG GGA AAT GCA ATC AAA TTA TGT GAT TGC GTC	431
Pro Leu Val Pro Ser Leu Gly Asn Ala Ile Lys Leu Cys Asp Cys Val	
130 135 140	
ACG GTC CCA CTT TTT TCA CTT CAA GTG ACG TTT TTT CCG GGC TCG GGT	479
Thr Val Pro Leu Phe Ser Leu Gln Val Thr Phe Phe Pro Gly Ser Gly	
145 150 155	

ATA TCA CTA GGA ATG ACG AAT CAT CAT AGC CTT GGT GAC GCT AGC ACG	527
Ile Ser Leu Gly Met Thr Asn His His Ser Leu Gly Asp Ala Ser Thr	
160 165 170 175	
CGG TTC AAC TTT TTG AAA GGG TGG ACT TCG ATT ATT CAA TCT GGT GTA	575
Arg Phe Asn Phe Leu Lys Gly Trp Thr Ser Ile Ile Gln Ser Gly Val	
180 185 190	
GAT CGG TCT TTT TTA ACG AAA GGA TCT CCA CCG GTT TTT GAT AGA TTG	623
Asp Arg Ser Phe Leu Thr Lys Gly Ser Pro Pro Val Phe Asp Arg Leu	
195 200 205	
ATT AAC ATC CCA CAT TTA GAT GAA AAT AAG TTG AGA CAT ACA AGG CTC	671
Ile Asn Ile Pro His Leu Asp Glu Asn Lys Leu Arg His Thr Arg Leu	
210 215 220	
GAA AGT TTT TAT AAA CCT TCG AGC CTT GTT GGT CCC ACT GAT AAA GTT	719
Glu Ser Phe Tyr Lys Pro Ser Ser Leu Val Gly Pro Thr Asp Lys Val	
225 230 235	
CGG TCA ACG TTT GTG TTG ACC CGA ACT AAT ATC AAT CTA CTA AAG AAA	767
Arg Ser Thr Phe Val Leu Thr Arg Thr Asn Ile Asn Leu Leu Lys Lys	
240 245 250 255	
AAG GTC TTA ACC CAA GTG CCA AAC TTG GAG TAC ATG TCA TCT TTT ACG	815
Lys Val Leu Thr Gln Val Pro Asn Leu Glu Tyr Met Ser Ser Phe Thr	
260 265 270	
GTA ACT TGT GGT TAT ATA TGG AGT TGC ATA GCG AAA TCA CTC GTA AAA	863
Val Thr Cys Gly Tyr Ile Trp Ser Cys Ile Ala Lys Ser Leu Val Lys	
275 280 285	
ATA GGA GAA AGA AAG GGC GAA GAC GAG TTA GAA CAG TTC ATA ATC ACC	911
Ile Gly Glu Arg Lys Gly Glu Asp Glu Leu Glu Gln Phe Ile Ile Thr	
290 295 300	
ATT GAT TGT CGA TCT CGT CTT GAT CCA CCA ATT CCC ACA GCC TAC TTT	959
Ile Asp Cys Arg Ser Arg Leu Asp Pro Pro Ile Pro Thr Ala Tyr Phe	
305 310 315	
GGT AAC TGT GGT GCA CCA TGT GTC CCG ACC TTA AAA AAT GTC GTT TTG	1007
Gly Asn Cys Gly Ala Pro Cys Val Pro Thr Leu Lys Asn Val Val Leu	
320 325 330 335	
ACT AGC GAA AAT GGG TAT GCA CTT GGT GCT AAA GTA ATT GGA GAG TCT	1055
Thr Ser Glu Asn Gly Tyr Ala Leu Gly Ala Lys Val Ile Gly Glu Ser	
340 345 350	

ATA TGC AAA ATG ATA TAT AAT AAG GAC GGA ATC TTG AAA GAT GCC GCG 1103  
Ile Cys Lys Met Ile Tyr Asn Lys Asp Gly Ile Leu Lys Asp Ala Ala  
355 360 365  
AGA TGG CAT GAA CCT TTC ATG ATC CCG GCT AGG AAG ATT GGT GTT GCT 1151  
Arg Trp His Glu Pro Phe Met Ile Pro Ala Arg Lys Ile Gly Val Ala  
370 375 380  
GGT ACA CCT AAG CTC AAC TTG TAC GAC TTT GAT TTT GCG TGG GGG AAG 1199  
Gly Thr Pro Lys Leu Asn Leu Tyr Asp Phe Asp Phe Gly Trp Gly Lys  
385 390 395  
CCG ATA AAG TAT GAG ACT GTT TCA ATA GAC TAT AAT ACG TCG ATT TCT 1247  
Pro Ile Lys Tyr Glu Thr Val Ser Ile Asp Tyr Asn Thr Ser Ile Ser  
400 405 410 415  
ATA AAT GCA AGC AAA ACA TCA GCA CAA GAT CTT GAA ATT GGA TTG AGT 1295  
Ile Asn Ala Ser Lys Thr Ser Ala Gln Asp Leu Glu Ile Gly Leu Ser  
420 425 430  
CTA CCG AGT ATG CAA ATG GAG GCG TTT TCT AGC ATC TTT GAT GAA GGA 1343  
Leu Pro Ser Met Gln Met Glu Ala Phe Ser Ser Ile Phe Asp Glu Gly  
435 440 445  
TTA GAG AGT CAA GTT TCA TTG TAGATCATCG TCCCCTTTTT GTGTGCATCA 1394  
Leu Glu Ser Gln Val Ser Leu  
450 454  
AGTTTCTGTC GTTTTATGA GTTGCCACTG TTCTATTCTT TAAGTATACC TTTCGACTAT 1454  
GTTTGAAGA TGCAACGATA TAAAATGAAA AAAAAAAAAA AAAAAAAAAA AAAA 1508

SEQ ID NO: 6

SEQUENCE LENGTH: 1521

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL SEQUENCE: No

ANTI-SENSE: No

ORIGINAL SOURCE

ORGANISM: *Lavandula angustifolia*

TISSUE TYPE: petal

IMMEDIATE SOURCE

LIBRARY: cDNA library

CLONE: pLAT21

# SEQUENCE DESCRIPTION

-TG ACC ACC CTC CTC GAA TCC TCC CGA GTG GCG CCG CCT CCA GGC ACG	47
Xxx Thr Thr Leu Leu Glu Ser Ser Arg Val Ala Pro Pro Pro Gly Thr	
1 5 10 15	
GTG GCT GAG CAG TCA CTC CCG CTC ACC TTC TTC GAC ATG ACG TGG CTG	95
Val Ala Glu Gln Ser Leu Pro Leu Thr Phe Phe Asp Met Thr Trp Leu	
20 25 30	
CAT TTC CAC CCC ATG CTT CAG CTT CTC TTC TAC GAA CTC CCC TGT TCC	143
His Phe His Pro Met Leu Gln Leu Leu Phe Tyr Glu Leu Pro Cys Ser	
35 40 45	
AAA CCC GCC TTC CTC GAA ACC GTC GTT CCG AAA CTC AAA CAA TCC TTA	191
Lys Pro Ala Phe Leu Glu Thr Val Val Pro Lys Leu Lys Gln Ser Leu	
50 55 60	
TCT CTA ACC CTC AAA CAC TTC TTC CCC CTT TCA TGC AAT CTA ATC TAC	239
Ser Leu Thr Leu Lys His Phe Phe Pro Leu Ser Cys Asn Leu Ile Tyr	
65 70 75	
CCT CTA TCG CCG GAG AAA ATG CCG GAG TTC CGG TAT CAG AAC GGT GAC	287
Pro Leu Ser Pro Glu Lys Met Pro Glu Phe Ser Val Ser Phe Thr Ile	
80 85 90 95	
TCG GTT TCT TTC ACG ATT ATG GAG TCT GTC GGA GAT CAT CCG CAT TCC	335
Met Glu Ser Ser Asp Asp Tyr Glu Asp Val Gly Asp His Pro His Ser	
100 105 110	
GCT CAT AAA TAC TAC TGC TTT GCC CCT AGC GAC GAT TAT GAA GAT CTC	383
Ala His Lys Tyr Tyr Cys Phe Ala Gln Leu Pro Pro Ile Val Glu Glu	
115 120 125	
CAG CTG CCG CCG ATA GTC GAG GAA TCT GAT CGG AAA TTG TTT CAA GTT	431
Ser Asp Arg Lys Leu Phe Gln Val Pro Leu Arg Tyr Gln Asn Gly Asp	
130 135 140	
TTA GCC GTG CAA GTG ACT CTG TTT CCC GGT CGC GGG GTG TGC ATC GGA	479
Leu Ala Val Gln Val Thr Leu Phe Pro Gly Arg Gly Val Cys Ile Gly	
145 150 155	
ATA ACG ACG CAC CAC ACC GTT AGC GAT GCT CCA TCG TTT GTA GGG TTT	527
Ile Thr Thr His His Thr Val Ser Asp Ala Pro Ser Phe Val Gly Phe	
160 165 170 175	
ATG AAG AGT TGG GCT TCC ATC ACT AAA TTC GGA GGA GAT GAT GAA TTC	575
Met Lys Ser Trp Ala Ser Ile Thr Lys Phe Gly Gly Asp Asp Glu Phe	
180 185 190	



TTG GAC GGA AAA GGT GAA TGT TTG CCG GTT TTC GAC CGA TCG CTC GTG	623
Leu Asp Gly Lys Gly Glu Cys Leu Pro Val Phe Asp Arg Ser Leu Val	
195 200 205	
AAT TAT CCG CCT AAA TTG GAC ACA TAT TTA TGG AAC AAC GCG CAG AAA	671
Asn Tyr Pro Pro Lys Leu Asp Thr Tyr Leu Trp Asn Asn Ala Gln Lys	
210 215 220	
CGT CCG TTG GAA TCG CAG CAT CCA TCT TTA CCG ACG GAT CGG ATT CGA	719
Arg Pro Leu Glu Ser Gln His Pro Ser Leu Pro Thr Asp Arg Ile Arg	
225 230 235	
GCT ACC TAC CTT TTC ACC CAA TCT GAA ATT AAG AAA TTG AAG GGT TTG	767
Ala Thr Tyr Leu Phe Thr Gln Ser Glu Ile Lys Lys Leu Lys Gly Leu	
240 245 250 255	
ATT CAG AGA AAA GCC CCA AAT GTA GTT AAT CTC TCT TCC TTC GTC GCG	815
Ile Gln Arg Lys Ala Pro Asn Val Val Asn Leu Ser Ser Phe Val Ala	
260 265 270	
ATC GCA GCT TAT ATC TGG ACC GGC ATC GCC AAA TCG GTC GGA GAT TAC	863
Ile Ala Ala Tyr Ile Trp Thr Gly Ile Ala Lys Ser Val Gly Asp Tyr	
275 280 285	
AAA GAC GTG GAT GAC GAC AAA CGC GCT TTC TTT TTA ATT CCG ATC GAT	911
Lys Asp Val Asp Asp Asp Lys Arg Ala Phe Phe Leu Ile Pro Ile Asp	
290 295 300	
TTA AGG CCG CGT TTG GAT CCG CCG GCT CCG GGG AAC TAC TTC GGA AAC	959
Leu Arg Pro Arg Leu Asp Pro Pro Ala Pro Gly Asn Tyr Phe Gly Asn	
305 310 315	
TGT CTA TCG TTT GCG ATG GCG AAG ATC CTG CGG CGG GAT TTG GTC GGA	1007
Cys Leu Ser Phe Ala Met Ala Lys Ile Leu Arg Arg Asp Leu Val Gly	
320 325 330 335	
GAT GAA GGG GTG TTT CGG GCA GCT GAG GCG ATC GCG GCG GAA ATA GAG	1055
Asp Glu Gly Val Phe Arg Ala Ala Glu Ala Ile Ala Ala Glu Ile Glu	
340 345 350	
AAG AGG ACG AGC GAC AAG AAG ATT CTA GAA ACT GTG GAG AAC TGG CCG	1103
Lys Arg Thr Ser Asp Lys Lys Ile Leu Glu Thr Val Glu Asn Trp Pro	
355 360 365	
TCT GAG ATT CGC GAA GCC TTG CAA AAC TGT TAT TTC TCG GTG GCG GGA	1151
Ser Glu Ile Arg Glu Ala Leu Gln Asn Cys Tyr Phe Ser Val Ala Gly	
370 375 380	

TCG AGC AGG CTT GAT CTT TAC GGC GCG GAT TTT GGA TGG GGT AAG GCG	1199
Ser Ser Arg Leu Asp Leu Tyr Gly Ala Asp Phe Gly Trp Gly Lys Ala	
385 390 395	
GTG AAG CAA GAG ATA CTG TCG ATT GAT GGA GAG AAG TTT ACG ATG TCG	1247
Val Lys Gln Glu Ile Leu Ser Ile Asp Gly Glu Lys Phe Thr Met Ser	
400 405 410 415	
TTG TGT AAA CCG AGG GAT GCT GCC GGA GGA TTG GAG GTT GGA TTG TCT	1295
Leu Cys Lys Pro Arg Asp Ala Ala Gly Gly Leu Glu Val Gly Leu Ser	
420 425 430	
TTG CCA AAG GAG GAA TTG CAA GCT TTT GAT GAT TAT TTT GCG GAG GGA	1343
Leu Pro Lys Glu Glu Leu Gln Ala Phe Asp Asp Tyr Phe Ala Glu Gly	
435 440 445	
ATA AAG GGT TGATTAATCA TTTAATCATG TATTATGAAG TTGGATGAAA	1392
Ile Lys Gly	
450	
TCCTCTGTTT CATCTCTATT GTTTAAACAA TAATTTTTTTT CCATTGAACT TTTTGTAGTC	1452
AATAAAAAAAAA AAAAAAAAAA AAAAAAATG AAAAAACTCA GTTATTTTTT TTTTTTTTTT	1512
TTTTTTTTT	1521

SEQ ID NO: 7

SEQUENCE LENGTH: 10

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Arg Phe Leu Gly Ile Thr Gly Ser Pro Lys

1 5 10

SEQ ID NO: 8

SEQUENCE LENGTH: 8

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Ile His Met Asp Ala Phe Ala Lys

1 5

SEQ ID NO: 9

SEQUENCE LENGTH: 10  
SEQUENCE TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL SEQUENCE: No  
SEQUENCE DESCRIPTION

Gly Val Glu Ile Gly Val Ser Leu Pro Lys  
1 5 10

SEQ ID NO: 10  
SEQUENCE LENGTH: 8  
SEQUENCE TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL SEQUENCE: No  
SEQUENCE DESCRIPTION  
Ala Ser Leu Ser Leu Thr Leu Lys  
1 5

SEQ ID NO: 11  
SEQUENCE LENGTH: 14  
SEQUENCE TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL SEQUENCE: No  
SEQUENCE DESCRIPTION  
His Tyr Val Pro Leu Ser Gly Asn Leu Leu Met Pro Ile Lys  
1 5 10

SEQ ID NO: 12  
SEQUENCE LENGTH: 14  
SEQUENCE TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL SEQUENCE: No  
SEQUENCE DESCRIPTION  
Val Arg Ala Thr Tyr Val Leu Ser Leu Ala Glu Ile Gln Lys  
1 5 10

SEQ ID NO: 13  
SEQUENCE LENGTH: 8

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Ile His Met Asp Ala Phe Ala Lys

1 5

SEQ ID NO: 14

SEQUENCE LENGTH: 9

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Lys Ile His Met Asp Ala Phe Ala Lys

1 5

SEQ ID NO: 15

SEQUENCE LENGTH: 8

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Lys Ile His Met Asp Ala Phe Ala

1 5

SEQ ID NO: 16

SEQUENCE LENGTH: 23

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

AARATHCAYA TGGAYGCITT YGC

SEQ ID NO: 17

SEQUENCE LENGTH: 23

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

CTCGAGTTTT TTTTTTTTTT TTT

23

SEQ ID NO: 18

SEQUENCE LENGTH: 26

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

TTCACCATGG AGCAAATCCA AATGGT

26

SEQ ID NO: 19

SEQUENCE LENGTH: 17

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

CGAGTCGCCC TCATCAC

17

SEQ ID NO: 20

SEQUENCE LENGTH: 16

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

AACAGCTATG ACCATG

16

SEQ ID NO: 21

SEQUENCE LENGTH: 6

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide  
HYPOTHETICAL SEQUENCE: No  
SEQUENCE DESCRIPTION  
Asp Phe Gly Trp Gly Lys

1 5

SEQ ID NO: 22  
SEQUENCE LENGTH: 17  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA  
HYPOTHETICAL SEQUENCE: No  
SEQUENCE DESCRIPTION  
GAYTTYGGIT GGGGIAA

17

SEQ ID NO: 23  
SEQUENCE LENGTH: 21  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA  
HYPOTHETICAL SEQUENCE: No  
SEQUENCE DESCRIPTION  
TGGCAACTGT CTTGCGTCAT G

21

SEQ ID NO: 24  
SEQUENCE LENGTH: 23  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA  
HYPOTHETICAL SEQUENCE: No  
SEQUENCE DESCRIPTION  
CCATGTCAGG TGTGAGGTTC AAC

23

SEQ ID NO: 25  
SEQUENCE LENGTH: 20  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

ATCGTTTCGC ATGATTGAAC

20

SEQ ID NO: 26

SEQUENCE LENGTH: 20

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

TCAGAAGAAC TCGTCAAGAA

20

SEQ ID NO: 27

SEQUENCE LENGTH: 53

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

GGGATCCAAC A ATG GAG CAA ATC CAA ATG GTG GCC GTG ATC GAA ACG TGT

50

Met Glu Gln Ile Gln Met Val Ala Val Ile Glu Thr Cys

1

5

10

AGA

53

Arg

15

SEQ ID NO: 28

SEQUENCE LENGTH: 16

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

GTAAAACGAC GGCCAT

16

SEQ ID NO: 29

SEQUENCE LENGTH: 45

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

GGGATCCAAC A ATG GAG CAA ATC CAA ATG GTG AAC ATT CTC GAA C

45

Met Glu Gln Ile Gln Met Val Asn Ile Leu Glu

1

5

10

SEQ ID NO: 30

SEQUENCE LENGTH: 21

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

CTCGGAGGAA TTCGGCACGA C

21

SEQ ID NO: 31

SEQUENCE LENGTH: 35

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

AGTCGGATCC AACA ATG ACC ACC CTC CTC GAA TCC

35

Thr Thr Leu Leu Glu Ser

1

5